



attachment #4

SEQUENCE LISTING

<110> BROUN, Pierre
VAN DE LOO, Frank
BODDUPALLI, Sekhar
SOMERVILLE, Chris

<120> PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY
MODIFIED PLANTS

<130> 20263/255164

<140> 09/117,921

<141> 1999-03-04

<150> 08/597,313

<151> 1996-02-06

<150> PCT/US97/02187

<151> 1997-02-06

<160> 15

<170> MS Word

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<211> 543

<212> DNA

<213> Lesquerella fendleri

<220>

<221> UNSURE

<222> 83

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<400> 1

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gaccgtgaac gtctccagat atacatctca gatgctggta ttctagctgt ctggttatgg 300
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cttttgatag tgaacttttt ccttgtcttg gtcactttct tgcagcacac tcatccttca 420
ttacctcact atgattcaac cgagtgggaa tggattagag gagctttggg tacggtagac 480
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<213> Lesquerella fendleri

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atcatgatgt taactgtcca gtctgtcttc ggttggccct tgtacttagc cttcaacgtt 180
tctggcagac cctacaatgg ttctgcttcc catttcttcc ccaatgctcc tatctacaac 240
gaccgtgaac gcctccagat ttacatctct gatgctggta ttctagccgt ctggttatgg 300
ctttaccgtt acgctgttgc acaaggacta gcctcaatga tctgtctaaa cggagtcccg 360
cttctgatag ttaacttttt cctcgtcttg atcacttact tacaacacac tcaccctgcg 420
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 cact 544

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 <212> DNA
 <213> Lesquerella fendleri

<220>
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 <222> 46, 99, 203, 1658, 1788
 <223> any

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 gccacccatt ttggacccac ganccttcca tttaaaccct ctctcgtgct attcaccaga 240
 agagaagcca agagagagag agagagaatg ttctgaggat cattgtcttc ttcacgttta 300
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 taatgggttac cccctcttcc aagaaatcag aaactgaagc cctaaaacgt ggaccatgtg 480
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 <211> 384
 <212> PRT
 <213> Lesquerella fendleri

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Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser
 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
 65 70 75 80
 Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys
 85 90 95
 Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala
 100 105 110
 Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His
 115 120 125
 Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg
 130 135 140
 His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro
 145 150 155 160
 Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro
 165 170 175
 Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro
 180 185 190
 Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala
 195 200 205
 Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp
 275 280 285
 Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp
 340 345 350

Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro
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 Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu
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 <211> 387
 <212> PRT
 <213> Ricinus communis

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 35 40 45
 Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
 50 55 60
 Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
 65 70 75 80
 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
 85 90 95
 Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
 100 105 110
 His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
 115 120 125
 Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
 130 135 140
 His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
 145 150 155 160
 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
 165 170 175
 Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
 180 185 190
 Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
 195 200 205
 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
 210 215 220
 Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
 225 230 235 240
 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
 245 250 255

Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
 260 265 270
 Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
 275 280 285
 Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
 290 295 300
 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
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 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
 325 330 335
 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
 340 345 350
 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
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 Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
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 Asn Lys Tyr
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 <211> 383
 <212> PRT
 <213> Arabidopsis thaliana

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 Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
 65 70 75 80
 Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 165 170 175
 Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
 195 200 205
 His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
 210 215 220
 Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr
 225 230 235 240
 Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly
 245 250 255
 Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
 260 265 270
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
 275 280 285
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
 290 295 300
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
 305 310 315 320
 Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile
 325 330 335
 Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr
 340 345 350
 Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
 355 360 365
 Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu
 370 375 380

<210> 7
 <211> 383
 <212> PRT
 <213> Brassica napus

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 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45

Ile Pro Arg Ser Phe Ser His Leu Ile Trp Asp Ile Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His Ala Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Arg
 145 150 155 160
 Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser Thr Ser Thr Thr Phe Gly
 165 170 175
 Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr
 180 185 190
 Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys
 195 200 205
 His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
 210 215 220
 Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu
 225 230 235 240
 Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg
 245 250 255
 Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu
 260 265 270
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
 275 280 285
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
 290 295 300
 Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu
 305 310 315 320
 Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
 325 330 335
 Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val
 340 345 350
 Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
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Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

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 <211> 309
 <212> PRT
 <213> Glycine max

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 Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu
 35 40 45
 Leu Thr Arg Val Cys Gly His His Ala Phe Ser Lys Tyr Gln Trp Val
 50 55 60
 Asp Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val Pro Tyr
 65 70 75 80
 Phe Ser Trp Lys Ile Ser His Arg Arg His His Ser Asn Thr Gly Ser
 85 90 95
 Leu Asp Arg Asp Glu Arg Val Lys Val Ala Trp Phe Ser Lys Tyr Leu
 100 105 110
 Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile
 115 120 125
 Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
 130 135 140
 Ser Phe Ala Ser His Tyr His Pro Tyr Arg Val Arg Leu Leu Ile Tyr
 145 150 155 160
 Val Ser Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val
 165 170 175
 Ala Thr Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro
 180 185 190
 Leu Leu Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Arg Val
 195 200 205
 His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr
 210 215 220
 Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr
 225 230 235 240
 Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His
 245 250 255
 Leu Arg Val Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp Thr
 260 265 270

Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr Val
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Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg Asn
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Lys Tyr Leu Arg Val
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<210> 9
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 <212> PRT
 <213> Glycine max

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 35 40 45

Trp Val Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly
 50 55 60

Leu Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr
 65 70 75 80

Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu
 85 90 95

Val Phe Val Pro Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg
 100 105 110

Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu Tyr Leu
 115 120 125

Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr
 130 135 140

Asp Pro Tyr Gly Pro Ile Tyr Ser Val Ile Ser Asp Ala Gly Val Leu
 145 150 155 160

Ala Val Val Tyr Gly Leu Phe Arg Leu Ala Met Ala Lys Gly Leu Ala
 165 170 175

Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu Val Val Asn Gly Phe
 180 185 190

Leu Val Leu Ile Thr Phe Leu Gln His Thr His Val Ser Glu Trp Asp
 195 200 205

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
 210 215 220

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
 225 230 235 240

Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp
225 230 235 240

Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp
245 250 255

Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His
260 265 270

Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met
275 280 285

Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp
290 295 300

Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
305 310 315 320

Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His
325 330 335

Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu
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Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn
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Lys Lys Phe
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<210> 11
<211> 224
<212> PRT
<213> Ricinus communis

<400> 11
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Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr
35 40 45

Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Ser
50 55 60

Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met
65 70 75 80

Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe
85 90 95

Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro
100 105 110

Tyr Gly Pro Ile Tyr Asn Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser
115 120 125

Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile
 130 135 140
 Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu
 145 150 155 160
 Val Val Asn Ser Phe Leu Val Leu Ile Thr Phe Leu Gln His Thr His
 165 170 175
 Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly
 180 185 190
 Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe
 195 200 205
 His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro
 210 215 220

<210> 12
 <211> 20
 <212> DNA
 <213> Ricinus communis

<400> 12
 gctcttttgt gcgctcattc 20

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: homologous
 regions of Ricinus communis deduced by hydroxylase
 sequence and Arabidopsis thaliana deduced desaturase
 sequence for use as oligonucleotide primer

<400> 13
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<210> 14
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: homologous
 regions of Ricinus communis deduced by hydroxylase
 sequence and Arabidopsis thaliana deduced
 desaturase sequence for use as oligonucleotide primer

<220>
 <221> UNSURE
 <222> 6, 12, 15
 <223> any

<400> 14
 taywsncaym gnmgnca yca 20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: homologous
regions of Ricinus communis deduced by hydroxylase
sequence and Arabidopsis thaliana deduced
desaturase sequence for use as oligonucleotide primer

<220>
<221> UNSURE
<222> 7, 10, 16
<223> any

<400> 15
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21